

SEQUENCE ALIGNMENT -

SEQ ID NO: 1 VS SEQ ID NO: 3

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 5, 2003, 11:43:46 ; Search time 20 Seconds
(without alignments)
4.028 Million cell updates/sec

Title: us-10-090-516-3
Perfect score: 4875
Sequence: 1 atggacgtgaaggagaggaa.....ctactgggatgcccctctga 4875

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 1 seqs, 8262 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-10-090-516-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4874	100.0	8262	1 us-10-090-516-1	

ALIGNMENTS

RESULT 1
us-10-090-516-1

Query Match 100.0%; Score 4874; DB 1; Length 8262;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4874; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGC	60
Db	1	ATGGACGTGAAGGAGAGGAAGCCTTACCGCTCGCTGACCCGGCGCCGCGACGCCGAGCGC	60
Qy	61	CGCTACACCAGCTCGTCCGCGGACAGCGAGGAGGGCAAAGCCCCGAGAAATCGTACAGC	120
Db	61	CGCTACACCAGCTCGTCCGCGGACAGCGAGGAGGGCAAAGCCCCGAGAAATCGTACAGC	120
Qy	121	TCCAGCGAGACCCCTGAAGGCCTACGACAGGACGCCCGCTAGCCTATGGCAGCCGCGTC	180
Db	121	TCCAGCGAGACCCCTGAAGGCCTACGACAGGACGCCCGCTAGCCTATGGCAGCCGCGTC	180
Qy	181	AAGGACATTGTGCCGAGGAGGCCGAGGAATTCTGCCGCACAGGTGCCAACTTACCCTG	240
Db	181	AAGGACATTGTGCCGAGGAGGCCGAGGAATTCTGCCGCACAGGTGCCAACTTACCCTG	240
Qy	241	CGGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTACGGGACCCCTGTACCGGACAGACATT	300

Db 241 CGGGAGCTGGGGCTGGAAGAAGTAACGCCCCCTCACGGGACCCTGTACCGGACAGACATT 300
 Qy 301 GGCCTCCCCCACTGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360
 |||||
 Db 301 GGCCTCCCCCACTGCGGCTACTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGAC 360
 Qy 361 ACGGTGCTGTCCCCTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGGCGC 420
 |||||
 Db 361 ACGGTGCTGTCCCCTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGGCGC 420
 Qy 421 AGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 480
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 Db 421 AGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGACACCGAGCATGAA 480
 Qy 481 AACACTGAGACTGATCATCCGGGCGGCCTGCAGAACACGCGCGGCTCCGGACGCGCGCG 540
 |||||
 Db 481 AACACTGAGACTGATCATCCGGGCGGCCTGCAGAACACGCGCGGCTCCGGACGCGCGCG 540
 Qy 541 CCGCCGCTCTCGCACGCCCACACCCCAACCAGCACCACGCGGCCTCCATTAACCTCCCTG 600
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 Db 541 CCGCCGCTCTCGCACGCCCACACCCCAACCAGCACCACGCGGCCTCCATTAACCTCCCTG 600
 Qy 601 AACCAGGGGCAACTTCACGCCGAGGAGCAACCCAGCCCGGCCCCACGGACCACTCGCTC 660
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 Db 601 AACCAGGGGCAACTTCACGCCGAGGAGCAACCCAGCCCGGCCCCACGGACCACTCGCTC 660
 Qy 661 TCCGGAGAGCCCCCTGCCGCGGCGCCAGGAGCCTGCCACGCCCAGGAGAACTGGCTG 720
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 Db 661 TCCGGAGAGCCCCCTGCCGCGGCGCCAGGAGCCTGCCACGCCCAGGAGAACTGGCTG 720
 Qy 721 CTCAACAGCAACATCCCCCTGGAGACCAGAAACCTAGGCAAGCAGCCATTCTTAGGGACA 780
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 Db 721 CTCAACAGCAACATCCCCCTGGAGACCAGAAACCTAGGCAAGCAGCCATTCTTAGGGACA 780
 Qy 781 TTGCAGGACAACCTCATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGGCTTAC 840
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 Db 781 TTGCAGGACAACCTCATTGAGATGGACATTCTCGGCGCCTCCCGCCATGATGGGGCTTAC 840
 Qy 841 AGTGACGGGCACCTTCTCTTCAAGCCTGGAGGCACCTCCCCGCTCTTCTGCACCACATCA 900
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 Db 841 AGTGACGGGCACCTTCTCTTCAAGCCTGGAGGCACCTCCCCGCTCTTCTGCACCACATCA 900
 Qy 901 CCAGGGTACCACTGACGTCCAGCACAGTGACTCTCCTCCGCCCCGACCCCTGCCCCGC 960
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 Db 901 CCAGGGTACCACTGACGTCCAGCACAGTGACTCTCCTCCGCCCCGACCCCTGCCCCGC 960
 Qy 961 AGCACCTTCGCCCCGCGGCCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAAGTGAAG 1020
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 Db 961 AGCACCTTCGCCCCGCGGCCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAAGTGAAG 1020
 Qy 1021 TGCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGCTGGCATACTTT 1080
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 Db 1021 TGCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCTGCTGGCATACTTT 1080
 Qy 1081 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGTAT 1140
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 Db 1081 GTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGCAGCCGATGGAGGGGCAGATGTAT 1140
 Qy 1141 GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCAGCGTCTCCCTATACCCC 1200
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 Db 1141 GAGATCACGGAGGACACAGCCAGCAGTTGGCCTGTGCCAACCAGCGTCTCCCTATACCCC 1200
 Qy 1201 TCAGGGGGCACTGGCTTAGAGACCCTGACAGGAAAGGCAAAGGAACCACAGAAGGAAAG 1260
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 Db 1201 TCAGGGGGCACTGGCTTAGAGACCCTGACAGGAAAGGCAAAGGAACCACAGAAGGAAAG 1260
 Qy 1261 CCCAGTAGTTTCTTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGG 1320
 |||||
 Db 1261 CCCAGTAGTTTCTTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGAAGG 1320
 Qy 1321 CGAGCTTCCAGAAGATTCTCTGGCACTTTCTGGAGATCTCAAGTGTTTCATAGACCAT 1380

Db	1321	CGAGCTTCCCAGAAGATTCCCTCCTGGCACTTCTGGAGATCTCAAGTGTTTCATAGACCAT	1380
Qy	1381	CCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTATGGC	1440
Db	1381	CCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGGCAGCCCTGGTTGGCATTATGGC	1440
Qy	1441	AGAAAAGGCCTCCCTCCTTCACATACACAGTTTGACTTTGTGGAGCTGTGGATGGCAGG	1500
Db	1441	AGAAAAGGCCTCCCTCCTTCACATACACAGTTTGACTTTGTGGAGCTGTGGATGGCAGG	1500
Qy	1501	AGGCTCCTAACCCAGGAGGCGCGGAGCCTAGAGGGGACCCGCGCCAGTCTCGGGGAACT	1560
Db	1501	AGGCTCCTAACCCAGGAGGCGCGGAGCCTAGAGGGGACCCGCGCCAGTCTCGGGGAACT	1560
Qy	1561	GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTGGATTAGGAATCTGGCAC	1620
Db	1561	GTGCCCCCTCCAGCCATGAGACAGGCTTCATCCAGTATTGGATTAGGAATCTGGCAC	1620
Qy	1621	TTGGCTTTTACAATGACGAAAGGAGTCAGAAGTGGTTTCCTTTCTCACCCTGCCATT	1680
Db	1621	TTGGCTTTTACAATGACGAAAGGAGTCAGAAGTGGTTTCCTTTCTCACCCTGCCATT	1680
Qy	1681	GAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATCTCTGGGACC	1740
Db	1681	GAGTCGGTGGATAACTGCCCCAGCAACTGCTATGGCAATGGTGACTGCATCTCTGGGACC	1740
Qy	1741	TGCCACTGCTTCCTGGGTTTCCTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCCGTGCTC	1800
Db	1741	TGCCACTGCTTCCTGGGTTTCCTGGGCCCCGACTGTGGCAGAGCCTCCTGCCCCGTGCTC	1800
Qy	1801	TGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGC	1860
Db	1801	TGTAGCGGAAATGGCCAATACATGAAAGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGC	1860
Qy	1861	GCTGAGTGCATGTGCCCCACCAACCAGTGTATCGATGTGGCCTGCAGCAACCATGGCACC	1920
Db	1861	GCTGAGTGCATGTGCCCCACCAACCAGTGTATCGATGTGGCCTGCAGCAACCATGGCACC	1920
Qy	1921	TGCATCACGGGCACCTGCATCTGCAACCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTG	1980
Db	1921	TGCATCACGGGCACCTGCATCTGCAACCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTG	1980
Qy	1981	GACTGCATGGACCCACATGTTTCAAGCCGGGGTGTCTGCGTGAGAGGCGAATGCCACTGC	2040
Db	1981	GACTGCATGGACCCACATGTTTCAAGCCGGGGTGTCTGCGTGAGAGGCGAATGCCACTGC	2040
Qy	2041	TCTGTGGGATGGGGAGGCACCAACTGCGAGACCCCGAGGCCACATGCTTAGACCAGTGT	2100
Db	2041	TCTGTGGGATGGGGAGGCACCAACTGCGAGACCCCGAGGCCACATGCTTAGACCAGTGT	2100
Qy	2101	TCAGGCCACGGAACCTTCCTCCCGGACACCGGGCTTTGCGAGCTGTGACCCAAGCTGGACT	2160
Db	2101	TCAGGCCACGGAACCTTCCTCCCGGACACCGGGCTTTGCGAGCTGTGACCCAAGCTGGACT	2160
Qy	2161	GGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTA	2220
Db	2161	GGACACGACTGTTCTATCGAGATCTGTGCTGCCGACTGTGGTGGCCATGGCGTGTGCGTA	2220
Qy	2221	GGGGGCACCTGCCGCTGCGAGGATGGCTGGATGGGGGCAGCCTGCGACCAGCGGGCCTGC	2280
Db	2221	GGGGGCACCTGCCGCTGCGAGGATGGCTGGATGGGGGCAGCCTGCGACCAGCGGGCCTGC	2280
Qy	2281	CACCCGCGCTGTGCCGAGCATGGGACCTGCCGCGACGGCAAGTGCAGTGCAGCCCTGGC	2340
Db	2281	CACCCGCGCTGTGCCGAGCATGGGACCTGCCGCGACGGCAAGTGCAGTGCAGCCCTGGC	2340
Qy	2341	TGGAATGGCGAACACTGCACCATCGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGA	2400
Db	2341	TGGAATGGCGAACACTGCACCATCGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAGA	2400

Qy	2401	TGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGC	2460
Db	2401	TGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGGCTGGAGAGGAGCTGGC	2460
Qy	2461	TGTGACACTTCCATGGAGACTGCCTGCGGTGACAGCAAAGACAATGATGGAGATGGCCTG	2520
Db	2461	TGTGACACTTCCATGGAGACTGCCTGCGGTGACAGCAAAGACAATGATGGAGATGGCCTG	2520
Qy	2521	GTGGACTGCATGGACCCTGACTGCTGCCTCCAGCCCCTGTGCCATATCAACCCGCTGTGC	2580
Db	2521	GTGGACTGCATGGACCCTGACTGCTGCCTCCAGCCCCTGTGCCATATCAACCCGCTGTGC	2580
Qy	2581	CTTGGCTCCCTAACCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTACAGCAG	2640
Db	2581	CTTGGCTCCCTAACCCTCTGGACATCATCCAGGAGACACAGGTCCTGTGTACAGCAG	2640
Qy	2641	AACCTACACTCCTTCTATGACCGCATCAAGTTCCTCGTGGGCAGGGACAGCACGCACATA	2700
Db	2641	AACCTACACTCCTTCTATGACCGCATCAAGTTCCTCGTGGGCAGGGACAGCACGCACATA	2700
Qy	2701	ATCCCCGGGGAGAACCCTTTGATGGAGGGCATGCTTGTGTTATTTCGTGGCCAAGTGATG	2760
Db	2701	ATCCCCGGGGAGAACCCTTTGATGGAGGGCATGCTTGTGTTATTTCGTGGCCAAGTGATG	2760
Qy	2761	ACATCAGATGGAACCCCCCTGGTTGGTGTGAACATCAGTTTGTCAATAACCCTCTCTTT	2820
Db	2761	ACATCAGATGGAACCCCCCTGGTTGGTGTGAACATCAGTTTGTCAATAACCCTCTCTTT	2820
Qy	2821	GGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCC	2880
Db	2821	GGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTCC	2880
Qy	2881	ATCATCCTGCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTGTGGCTGCCA	2940
Db	2881	ATCATCCTGCGGTTTCGAGCGGGCACCTTTTCATCACACAGGAGCACACCCTGTGGCTGCCA	2940
Qy	2941	TGGGATCGCTTCTTGTGTCATGGAACCATCATCATGAGACATGAGGAGAATGAGATTCCC	3000
Db	2941	TGGGATCGCTTCTTGTGTCATGGAACCATCATCATGAGACATGAGGAGAATGAGATTCCC	3000
Qy	3001	AGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACG	3060
Db	3001	AGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGACG	3060
Qy	3061	TCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCATTTGTGCCGAAATTCAGGCTTTGCAG	3120
Db	3061	TCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCATTTGTGCCGAAATTCAGGCTTTGCAG	3120
Qy	3121	GAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGGACCCCT	3180
Db	3121	GAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGGACCCCT	3180
Qy	3181	GGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCCCTCAACCTCATG	3240
Db	3181	GGCTACAAATCTGTCTGAGGATCAGCCTCACCCACCCGACCATCCCCCTCAACCTCATG	3240
Qy	3241	AAGGTGCACCTCATGGTAGCGGTGGAGGGCGCCTCTTCAGGAAGTGGTTCGCTGCAGCC	3300
Db	3241	AAGGTGCACCTCATGGTAGCGGTGGAGGGCGCCTCTTCAGGAAGTGGTTCGCTGCAGCC	3300
Qy	3301	CCAGACCTGTCCTATTATTTCATTGGGACAAGACAGACGTCTACAACCAGAAGGTGTTT	3360
Db	3301	CCAGACCTGTCCTATTATTTCATTGGGACAAGACAGACGTCTACAACCAGAAGGTGTTT	3360
Qy	3361	GGGCTTTTCTAGAAGCCTTTGTTTCCGTGGGTTATGAATATGAATCCTGCCAGATCTAATC	3420
Db	3361	GGGCTTTTCTAGAAGCCTTTGTTTCCGTGGGTTATGAATATGAATCCTGCCAGATCTAATC	3420
Qy	3421	CTGTGGGAAAAAAGAACAACAGTGCTGCAGGGCTATGAAATTGACGCGTCCAAGCTTGGA	3480
Db	3421	CTGTGGGAAAAAAGAACAACAGTGCTGCAGGGCTATGAAATTGACGCGTCCAAGCTTGGA	3480

Qy 3481 GGATGGAGCCTAGACAAACATCATGCCCTCAACATTCAAAGTGGCATCCTGCACAAAGGG 3540
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 Db 3481 GGATGGAGCCTAGACAAACATCATGCCCTCAACATTCAAAGTGGCATCCTGCACAAAGGG 3540
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Qy 3541 AATGGGGAGAACCAGTTTGTGTCTCAGCAGCCTCCTGTCTATTGGGAGCATCATGGGCAAT 3600
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 Db 3541 AATGGGGAGAACCAGTTTGTGTCTCAGCAGCCTCCTGTCTATTGGGAGCATCATGGGCAAT 3600
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Qy 3601 GGGCGCCGGAGAAGCATCTCCTGCCCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTC 3660
 |||||
 Db 3601 GGGCGCCGGAGAAGCATCTCCTGCCCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCTC 3660
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Qy 3661 CTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTC AAC 3720
 |||||
 Db 3661 CTGGCCCCAGTGGCCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTC AAC 3720
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Qy 3721 TACATTAGAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGCTGAGTCACAGT 3780
 |||||
 Db 3721 TACATTAGAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGCTGAGTCACAGT 3780
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Qy 3781 CCAGCACACAAATACTACCTGGCCACAGACCCCATGAGTGGGGCCGTCTTCCTTTCTGAC 3840
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 Db 3781 CCAGCACACAAATACTACCTGGCCACAGACCCCATGAGTGGGGCCGTCTTCCTTTCTGAC 3840
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Qy 3841 AGCAACAGCCGGCGGGTCTTTAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAG 3900
 |||||
 Db 3841 AGCAACAGCCGGCGGGTCTTTAAATCAAGTCCACTGTGGTGGTGAAGGACCTTGTCAAG 3900
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Qy 3901 AACTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCTCCCCTTTGATGACACTCGCTGC 3960
 |||||
 Db 3901 AACTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCTCCCCTTTGATGACACTCGCTGC 3960
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Qy 3961 GGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAATCCCAGGGGCATTACAGTGGAC 4020
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 Db 3961 GGGGATGGTGGGAAGGCCACAGAAGCCACACTCACCAATCCCAGGGGCATTACAGTGGAC 4020
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Qy 4021 AAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGAATGGG 4080
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 Db 4021 AAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGATCAGACGCATCGATCAGAATGGG 4080
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Qy 4081 ATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCGGCCACTCAGCTGTGAT 4140
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 Db 4081 ATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATCAGCCCGGCCACTCAGCTGTGAT 4140
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Qy 4141 TCTGTCATGGATATTTCCAGGTTACCTGGAGTGGCCACAGACTTAGCCATCAACCCA 4200
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 Db 4141 TCTGTCATGGATATTTCCAGGTTACCTGGAGTGGCCACAGACTTAGCCATCAACCCA 4200
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Qy 4201 ATGGACAACACTCACTTTATGTCCTCGACAACAATGTGGTCCTGCAAATCTCTGAAAACCA 4260
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 Db 4201 ATGGACAACACTCACTTTATGTCCTCGACAACAATGTGGTCCTGCAAATCTCTGAAAACCA 4260
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Qy 4261 CAGGTGCGCATTGTGCGCGGAGGCCATGCACTGCCAGGTCCCTGGCATTGACCACTTC 4320
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Qy 4321 CTGCTAAGCAAGGTGGCCATCCACGCAACCCTGGAGTCAGCCACCGCTTTGGCTGTTTCA 4380
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 Db 4321 CTGCTAAGCAAGGTGGCCATCCACGCAACCCTGGAGTCAGCCACCGCTTTGGCTGTTTCA 4380
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Qy 4381 CACAATGGGGTCCTGTATATTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAG 4440
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 Db 4381 CACAATGGGGTCCTGTATATTGCTGAGACTGATGAGAAAAAGATCAACCGCATCAGGCAG 4440
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Qy 4441 GTCACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGCCCCAGTGGCTGTGACTGTAAA 4500
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 Db 4441 GTCACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGCCCCAGTGGCTGTGACTGTAAA 4500
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Qy 4501 AATGATGCCAACTGTGATTGTTTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAGTTA 4560
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Db 4501 AATGATGCCAACTGTGATTGTTTTCTGGAGACGATGGTTATGCCAAGGATGCAAAGTTA 4560
Qy 4561 AATACCCCATCTTCCTTGGCTGTGTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGG 4620
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Db 4561 AATACCCCATCTTCCTTGGCTGTGTGTGCTGATGGGGAGCTCTACGTGGCCGACCTTGGG 4620
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Qy 4621 AACATCCGAATTCGGTTTATCCGGAAGAACAAGCCTTTCCTCAACACCCAGAACATGTAT 4680
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Db 4621 AACATCCGAATTCGGTTTATCCGGAAGAACAAGCCTTTCCTCAACACCCAGAACATGTAT 4680
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Qy 4681 GAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGATACCACCGGCAAGCACCTG 4740
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Db 4681 GAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTTTGATACCACCGGCAAGCACCTG 4740
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Qy 4741 TACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAACCTCACCTACACTGGGGACGGC 4800
      |||
Db 4741 TACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAACCTCACCTACACTGGGGACGGC 4800
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Qy 4801 GACATCACACTCATCACAGACAACAATGGCAACATGGTAAATGTCCGCCGAGACTCTACT 4860
      |||
Db 4801 GACATCACACTCATCACAGACAACAATGGCAACATGGTAAATGTCCGCCGAGACTCTACT 4860
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Qy 4861 GGGATGCCCCCTCTGA 4874
      |||
Db 4861 GGGATGCCCCCTCTGA 4874

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Search completed: May 5, 2003, 11:44:07
Job time : 21 secs

Paper copy of sequence listing indicates
SEQ ID NO:3 has "A" @ position 4875
and SEQ ID NO:1 has "G" @ position
4876. These nucleotides have been
inserted for clarity.